

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2003, 07:19:15 ; Search time 25.458 Seconds
(without alignments)
234.715 Million cell updates/sec

Title: US-09-787-082-6
Perfect score: 173
Sequence: 1 CKKGAKGKRLMYDCTGSCRSRKTRNG 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21.*
- 1: sp-archaea.*
 - 2: sp-bacteria.*
 - 3: sp-fungi.*
 - 4: sp-human.*
 - 5: sp-invertebrate.*
 - 6: sp-mammal.*
 - 7: sp-mhc.*
 - 8: sp-organelle.*
 - 9: sp-phage.*
 - 10: sp-plant.*
 - 11: sp-rodent.*
 - 12: sp-virus.*
 - 13: sp-vertebrate.*
 - 14: sp-unclassified.*
 - 15: sp-rvirus.*
 - 16: sp-bacteriap.*
 - 17: sp-archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	73.4	66	5 Q9N633	Q9N633 conus catus
2	127	73.4	66	5 Q9NCW6	Q9NCW6 conus catus
3	127	73.4	66	5 Q9NCW5	Q9NCW5 conus catus
4	127	73.4	66	5 Q9NCW3	Q9NCW3 conus catus
5	120	69.4	66	5 Q9NCW4	Q9NCW4 conus catus
6	120	69.4	66	5 Q9NCV5	Q9NCV5 conus catus
7	117	67.6	66	5 Q9NCV7	Q9NCV7 conus catus
8	116	67.1	66	5 Q9NCV6	Q9NCV6 conus catus
9	116	67.1	66	5 Q9NCV4	Q9NCV4 conus stria
10	116	67.1	66	5 Q9NCV0	Q9NCV0 conus stria
11	116	67.1	66	5 Q9NCV1	Q9NCV1 conus stria
12	115	66.5	66	5 Q9N628	Q9N628 conus catus
13	115	66.5	66	5 Q9N625	Q9N625 conus catus
14	115	66.5	66	5 Q9NCW2	Q9NCW2 conus catus
15	115	66.5	66	5 Q9NCV3	Q9NCV3 conus stria
16	115	66.5	66	5 Q9NCV2	Q9NCV2 conus stria

17	115	66.5	66	5	Q9NCV1	Q9NCV1 conus stria
18	114	65.9	66	5	Q9N6F7	Q9N6F7 conus catus
19	114	65.9	66	5	Q9NCW1	Q9NCW1 conus catus
20	104	60.1	66	5	Q9N6F8	Q9N6F8 conus catus
21	104	60.1	66	5	Q9NCW0	Q9NCW0 conus catus
22	104	60.1	66	5	Q9NCV9	Q9NCV9 conus catus
23	103	59.5	66	5	Q9NCV6	Q9NCV6 conus catus
24	95	54.9	66	5	Q9NCV8	Q9NCV8 conus catus
25	65.5	37.9	57	5	Q9N9H2	Q9N9H2 venerupis (
26	65.5	37.9	59	5	Q9N9H1	Q9N9H1 ruditaipes d
27	65.5	37.9	80	5	Q9BIV4	Q9BIV4 crassostrea
28	65.5	37.9	107	5	Q9NGI9	Q9NGI9 crassostrea
29	62.5	36.1	75	5	Q9UIN5	Q9UIN5 crassostrea
30	61	35.3	541	4	Q9H6L0	Q9H6L0 homo sapien
31	60	34.7	81	5	Q9BP83	Q9BP83 conus arena
32	59	34.1	78	5	Q9U656	Q9U656 conus texti
33	59	34.1	401	13	P82942	P82942 naja naja k
34	59	34.1	686	5	Q94316	Q94316 caenorhabdi
35	58	33.5	78	5	Q9U655	Q9U655 conus texti
36	57.5	33.2	751	5	O01497	O01497 caenorhabdi
37	57.5	33.2	1368	5	Q23821	Q23821 caenorhabdi
38	57	32.9	67	5	Q9N604	Q9N604 conus stria
39	57	32.9	67	5	Q9NCU6	Q9NCU6 conus stria
40	57	32.9	67	5	Q9NCU3	Q9NCU3 conus stria
41	57	32.9	67	5	Q9NCU2	Q9NCU2 conus stria
42	57	32.9	2447	5	Q9NEF9	Q9NEF9 drosophila
43	57	32.9	4072	5	Q9W4Y4	Q9W4Y4 drosophila
44	56.5	32.7	105	13	O93517	O93517 agkistrodon
45	56.5	32.7	610	13	Q9DGB9	Q9DGB9 crotalus at

ALIGNMENTS

RESULT 1

Q9N633 PRELIMINARY; PRT; 66 AA.
AC Q9N633;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin precursor (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_11_6, CCATH_11_1, AND CCATH_11_2;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-eating Conus."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AFI74219; AAF89883.1; -
DR EMBL; AFI74214; AAF89878.1; -
DR EMBL; AFI74215; AAF89879.1; -
DR HSSP; P05484; 1MVI.
DR InterPro: IPR004214; Conotoxin.
DR Fram; PF02950; Conotoxin; 1.
FT NON_TER 1 1
SQ SEQUENCE 66 AA; 7053 MW; E445338A6968A1AC CRC64;

Query Match 73.4%; Score 127; DB 5; Length 66;
Best Local Similarity 80.0%; Pred. No. 6.3e-11;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CKKGAKGKRLMYDCTGSCRSRK 25

Db 41 CKKGASCRRTSYDCTGSCRSRGC 65

RESULT 2

Q9NCW6


```
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_R_4;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174238; AAF89902.1; -.
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7081 MW; 66E498A6968B31B CRC64;

Query Match 69.4%; Score 120; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 6.2e-10;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCCCTGSCRSRGC 25
   |:||| | | | | | | | | | | | |
DB 41 COGRGASCRKTSYDCCCTGSCRSRGC 65

RESULT 7
Q9NCV7 ID Q9NCV7 PRELIMINARY; PRT; 66 AA.
AC Q9NCV7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_R_2;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174236; AAF89900.1; -.
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7053 MW; 7453798A6968B31B CRC64;

Query Match 67.6%; Score 117; DB 5; Length 66;
Best Local Similarity 68.0%; Pred. No. 1.7e-09;
Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCCCTGSCRSRGC 25
   |:||| | | | | | | | | | | | |
DB 41 COGRGASCRKTSYDCCCTGSCRSRGC 65

RESULT 8
Q9N6N6 ID Q9N6N6 PRELIMINARY; PRT; 66 AA.
AC Q9N6N6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin precursor (Fragment).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
```

```
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSTRH_1_5, AND CSTRH_1_1;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174244; AAF89908.1; -.
DR EMBL; AF174240; AAF89904.1; -.
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 6966 MW; 29A992710CA7DA05 CRC64;

Query Match 67.1%; Score 116; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 2.3e-09;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCCCTGSCRSRGC 25
   |:||| | | | | | | | | | | | |
DB 41 CKAAGKSCSRITAYNCCCTGSCRSRGC 65

RESULT 9
Q9NCV4 ID Q9NCV4 PRELIMINARY; PRT; 66 AA.
AC Q9NCV4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSTRH_1_2;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174241; AAF89905.1; -.
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 6980 MW; 286F491D7CA7DA05 CRC64;

Query Match 67.1%; Score 116; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 2.3e-09;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCCCTGSCRSRGC 25
   |:||| | | | | | | | | | | | |
DB 41 CKAAGKSCSRITAYNCCCTGSCRSRGC 65

RESULT 10
Q9NCV0 ID Q9NCV0 PRELIMINARY; PRT; 66 AA.
AC Q9NCV0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN-CSTRH_1_7;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
   eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174226; AAF89893.1; -.
DR HSSP; P05484; 1MVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 6981 MW; 20CDC33D7CA7DA05 CRC64;

Query Match 67.1%; Score 116; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 2.3e-09;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGSCRSRGC 25
   || | ||| : ||||| |||||
Db 41 CRAAGKSCSRIAYNCTGSCRSRGC 65

RESULT 11
Q9NCU1 PRELIMINARY; PRT; 66 AA.
AC Q9NCU1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CSTRH_1_7;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
   eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174267; AAF89931.1; -.
DR HSSP; P05484; 1MVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 6951 MW; 0D9868C0A7A1A39F CRC64;

Query Match 67.1%; Score 116; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 2.3e-09;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGSCRSRGC 25
   || | ||| : ||||| |||||
Db 41 CRAAGKSCSRIAYNCTGSCRSRGC 65

RESULT 12
Q9N628 PRELIMINARY; PRT; 66 AA.
AC Q9N628;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Four-loop conotoxin precursor (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CCATH_111_9, AND CCATH_111_6;
RA Duda T.F., Palumbi S.R.;
```

```
RT "Molecular evolution of four-loop conotoxin precursors from fish-
   eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174229; AAF89893.1; -.
DR HSSP; P05484; 1MVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7057 MW; E7AA5E310968B7DA CRC64;

Query Match 66.5%; Score 115; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 3.2e-09;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGSCRSRGC 25
   || | ||| : ||||| |||||
Db 41 CKSTGASCRRTSYDCTGSCRSRGC 65

RESULT 13
Q9N625 PRELIMINARY; PRT; 66 AA.
AC Q9N625;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Four-loop conotoxin precursor (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
   eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174228; AAF89892.1; -.
DR EMBL; AF174221; AAF89885.1; -.
DR EMBL; AF174222; AAF89886.1; -.
DR EMBL; AF174224; AAF89888.1; -.
DR EMBL; AF174225; AAF89889.1; -.
DR HSSP; P05484; 1MVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7056 MW; EA11338A6968B7DA CRC64;

Query Match 66.5%; Score 115; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 3.2e-09;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGSCRSRGC 25
   || | ||| : ||||| |||||
Db 41 CKSTGASCRRTSYDCTGSCRSRGC 65

RESULT 14
Q9NCW2 PRELIMINARY; PRT; 66 AA.
AC Q9NCW2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
```

Search completed: March 17, 2003, 07:26:21
Job time : 25.458 secs

THIS PAGE BLANK (USPTO)